

REMARKS

Applicants have substituted into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-8.

Applicants have amended the previously filed Sequence Listing and revised Figures 1, 2A, 5, 7 and 8 to make them conform to the amended Sequence Listing.

SEQ ID NO:1 of the previously filed Sequence Listing corresponded to originally filed Figure 1. Originally filed Figure 1 erroneously duplicated the lower nucleotide sequence presented in Figure 4 (which lower sequence now corresponds to SEQ ID NO:4 in the attached substitute Sequence Listing). SEQ ID NO:1 of the Sequence Listing and Figure 1 have been amended to conform to the nucleotide sequence shown Figs. 2A (lower sequence), 5, 7 and 8. These amendments are supported by the disclosure in the specification of Figs. 1, 2A, 5, 7 and 8, that SEQ ID NO:1 is identical in all these figures.

The amendment to SEQ ID NO:2 was necessitated due to an erroneous addition of incorrect nucleotides at positions 886-953. These incorrect nucleotides have now been deleted from SEQ ID NO:2 and this amendment is supported by the nucleotide sequence shown in Figure 2A (upper sequence).

SEQ ID NO:3 has been deleted from the previously filed Sequence Listing as SEQ ID NO:3 was a partial sequence of SEQ ID NO:1. The subsequent sequences have been renumbered accordingly in the attached substitute Sequence Listing.

The revisions to Figs. 1, 2A and 5 were necessitated due to typographical/clerical errors made when drafting these figures, and were made to make the sequences of Figs. 1, 2A and 5 conform to SEQ ID NO:1.

The revisions to Figures 7 and 8 merely correct an alignment error in the second column of the last row of the sequence.

All of the above revisions to the Sequence Listing and the figures are of clerical/typographical nature and do not constitute new matter. Approval of all of the revisions is therefore respectfully requested.

Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.825(a) and 1.825(b).

I hereby state, in accordance with 37 C.F.R. §1.825(a), that the amendments included in the substitute sheets of the sequence listing are believed to be supported in the application as filed and that the substitute sheets of the sequence listing are not believed to include new matter.

I hereby further state, in accordance with 37 C.F.R. §1.825(b), that the attached copy of the computer readable form is the same as the attached substitute paper copy of the sequence listing.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADEIn the specification:

The table on page 15 has been amended as follows:

5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	SEQ ID NO:6
5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	SEQ ID NO:7
5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	SEQ ID NO:8
5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	SEQ ID NO:9
5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	SEQ ID NO:10
5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	SEQ ID NO:11
5' GAC CCC CAT TTG TGT GAC 3'	SEQ ID NO:12
5' CGA CGA CTC CTG GAG CCC G 3'	SEQ ID NO:13
5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	SEQ ID NO:14
5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	SEQ ID NO:15
5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	SEQ ID NO:16
5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	SEQ ID NO:17
5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	SEQ ID NO:18
5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	SEQ ID NO:19
5' CAT TTC GGG GAT TCG GGG GA 3'	SEQ ID NO:20
5' GGG GGA CGG AAC CCG GCG CT 3'	SEQ ID NO:21
5' CCC TCT ACA CTT ATC ATC TTC 3'	SEQ ID NO:22
5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	SEQ ID NO:23
5' GTC ACT ACT GGA ATT CCC TTC TCC 3'	SEQ ID NO:24
5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	SEQ ID NO:25
5' GGA AAT CGC TGT CGC CTA ACC 3'	SEQ ID NO:26
5' GGT TAG GCG ACA GCG ATT TCC 3'	SEQ ID NO:27
5' GGC CAC GCG TCG ACT AGT AC 3'	SEQ ID NO:28
5' GTA ATG CAC ACTCCA TTG GC 3'	SEQ ID NO:29
5' GTA ATG CAC ACT CCA TTG 3'	SEQ ID NO:30
5' GCG CTC AGC TGG AAT TCC 3'	SEQ ID NO:31
5' GGA ATT CCA GCT GAG CGC 3'	SEQ ID NO:32
5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3'	SEQ ID NO:33
5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	SEQ ID NO:34
5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	SEQ ID NO:35
5' CCC GCT CGA GTC AGG GTG ACC GAA AAA TCA G 3'	SEQ ID NO:36

The two paragraphs beginning at line 6 on page 16 and ending at line 13 of page 16 have been amended as follows:

**Fig. 1** shows the nucleic acid sequence (SEQ ID NO:1) of clone T16 isolated from T47D breast cancer cDNA library. Initiation and termination codons of the open reading frame are indicated by dark bars;

**Fig. 2A** shows a comparison of the nucleic acid sequences (upper sequence) (SEQ ID NO:2) of clone 4.7 isolated from a placenta cDNA library exhibiting normal human FTH, and the sequences (lower sequence) of clone T16 (SEQ ID NO:1) isolated from human breast cancer T47D cDNA library. Initiation and termination codons of the open reading frame are marked by dark boxes;

The three paragraphs beginning at line 17 of page 16 and ending at line 25 of page 16 have been amended as follows:

**Fig. 3** shows a comparison of sequence homology between cDNA clone T16 (residues 463-671 of SEQ ID NO:1) and human mitochondrial cytochrome oxidase I DNA (SEQ ID NO:3);

**Fig. 4** shows a comparison of nucleic acid sequences between placental cDNA obtained by PCR amplification using T16 specific primers (upper sequence) (residues 24-822 of SEQ ID NO:1) and T16 cDNA sequence obtained from the T16 cDNA clone (lower sequence) (SEQ ID NO:4). Identical nucleic acid sequences are indicated by a dotted line. Initiation and termination codons are indicated by a dark bar;

**Fig. 5** shows the nucleic acid sequence and deduced amino acid sequence (SEQ ID NO:5) of the cDNA of OFF1;

The two paragraphs beginning at line 4 of page 17 and ending at line 6 of page 17 have been amended as follows:

**Fig. 7** shows the sequence of clone T16 (SEQ ID NO:1).  
pPrimers used for PCR are indicated in the above sequence;

**Fig. 8** shows the restriction enzyme map sequence of clone T16 (SEQ ID NO:1);

Table 1 on page 19 has been amended as follows:

**Table 1**  
**List of Primers**

Name	#MR	Sequence	SEQ ID NO.		
1060F	24	5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	6	75%	
1061R	24	5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	7	45.80%	
17F	27	5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	8	52%	27618
X1.1F	24	5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	9	50%	24880
X.1.1R	24	5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	10	67%	
2.1F	24	5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	11	58%	
3.4F	18	5' GAC CCC CAT TTG TGT GAC 3'	12	55.50%	
1060F/S	19	5' CGA CGA CTC CTG GAG CCC G 3'	13	73.70%	
1061r/Bio	24	5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	14	45.80%	
16X.1R	24	5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	15	50%	24879
17R	27	5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	16	52%	27385
3'COD R	28	5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	17	50%	28313
5' NCF	24	5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	18	58%	24870
4869	27	5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	19	63%	
NFG	20	5' CAT TTC GGG GAT TCG GGG GA 3'	20	60%	
NFGP-2	20	5' GGG GGA CGG AAC CCG GCG CT 3'	21	80%	201880
767-F	21	5' CCC TCT ACA CTT ATC ATC TTC 3'	22	43%	211616
16-F	24	5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	23	50%	241173
ECO-F	24	5' GTC ACT ACT GGA ATT CCC TTC TCC 3'	24	50%	24960
ECO-R	24	5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	25	50%	24961
SPF	21	5' GGA AAT CGC TGT CGC CTA ACC 3'	26	57%	211667
SPR	21	5' GGT TAG GCG ACA GCG ATT TCC 3'	27	57%	211668
AUAP	20	5' GGC CAC GCG TCG ACT AGT AC 3'	28	65%	202738
NC-F	20	5' GTA ATG CAC ACTCCA TTG GC 3'	29	50%	203814
SNC-F	18	5' GTA ATG CAC ACT CCA TTG 3'	30	44%	181897
BNC-F	18	5' GCG CTC AGC TGG AAT TCC 3'	31	55.50%	181898
BNC-R	18	5' GGA ATT CCA GCT GAG CGC 3'	32	61.10%	181905
pGEX-F	29	5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC3'	33	67%	29391
pGEX-R1	27	5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	34	51.85%	27578
pGEX-R2	29	5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	35	51.70%	29396
pGEX-R3	31	5' CCCGCTCGAGTCAGGGTGACCGAAAAATCAG 3'	36	58%	31277



The paragraph beginning at line 6 on page 27 has been amended as follows:

The expression vector (pGEX-5X-1) used for gene fusion construction was the GST Gene Fusion System (Pharmacia). The OFF1 coding region (designated as "FL", full-length) of about 0.5 kb was prepared by PCR with the following 5' end primer:

5' GTGGGATCCCATGACGACCGCGTCCA (1-27 of SEQ ID NO:33), in order  
BamHI

to add a BamHI site 1 base upstream from the start codon ATG and with the 3' end primer

5' CCCG CTCGAG TCA GGG TGA CCG AAA AAT CAG 3' (SEQ ID NO:36) in  
XhoI

order to add an XhoI site after the stop codon TAA using the PCR kit (Perkin-Elmer/Cetus).

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5'	TTGACACCAG	ACCAACTGGT	AATGGTAGCC	ACGGGCGCTC	AGCTGG <sup>A</sup> ATT	CC <sup>AA</sup> AAAAATG
	TAATGCACAC	TCCATTG <del>A</del> CAT	TCAGCCCGCC	TCTCCTTAGT	CGCCGCCCATG	ACGACCCGGT
	CCACCTCCCA	GGTGCGCCAG	AACTACCACC	AGGACTCAGA	GGCCGCCATC	AACCGCCAGA
	TCAACCTGGA	GCTCTACGCC	TCCTACGTTT	ACCTGTCCAT	GTCTTACTAC	TTTGACCCGG
	ATGATGTGGC	TTTGAAGAAC	TTTGCCAAAT	ACTTTCTTCA	CCAATCTCAT	GAGGAGAGGG
	AACATGCTGA	GAAACTGATG	AAGCTGCAGA	ACCAACGAGG	TGGCCGAATC	TTCTTCAGG
	ATATCAAGAA	ACCAGACTGT	GATGACTGGG	AGAGCGGGCT	GAATGCAATG	GAGTGTGCAT
	TACATTGGGA	AAAAAATGTG	AATCAGTCAC	TACTGGAATT	CCCTTCTCCT	ATCTCTCCCA
	GTCTAGCTG	CTGGCATCAC	TATACTACTA	ACAGACCGCA	ACCTCAACAC	CACCTTCTTC
	GACCCCGCCG	GAGGAAGAGA	CCCCATTCTA	TACCAACACC	TATTCTGATT	TTTCGGTCAC
	CCTGA <sup>A</sup> AGTTT	ATATTCTTAT	CCTACCAGGC	TTCGGAATAA	TCTCCCATAT	TGTAACCTAC
	TACTCCGGAA	ATCGCTGTCG	CCTAACCGCT	AACATTACTG	CAGGCCACCT	ACTCATGCAC
	CTAATTGGAA	GCGCCACCCT	AGCAATATCA	ACCATTAACC	TTCCCTCTAC	ACTTATCATC
	TTCACAATTC	TAATTCTACT	GACTATCCTA	GAAATCGCTG	TCGCCTTAAT	CCAAGCCTAC
	GTTTTACAC	TTCTAGTAA <sup>G</sup>	<del>C</del> CCTCTACCT G	<del>C</del> CACGACAAC <sup>A</sup>	<del>C</del> CATAAAAAA <sup>A</sup>	<del>A</del> 3'

Fig. 1

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CLONE d47

GGGGGACGGAACCCGG

Fig. 2A

CGCTCGTTCCCCACCCCGGCCGGCCGCCCATAGCCAGCCCTCCGTAC

CLONE T 16

TTGACACCCX

CTCTTCACCGCACCCCTCGGACTGCCCAAGGCCCGCCGCGCTCC  
A<sup>6</sup>ACCAACTGGTAATGGTAGCGACCGGCGCTCAGCTGGAATTCCAAAAGCGCCGCGCAGCCACCGCCGCGCGCCGCGCCTCTCCTTAGTCGCCGCC  
AATGTAATGCACACTCCATTGCATTGACCCGCGCTCTCCTTAGTCGCCGCC

ATG	ACG	ACC	GCG	TCC	ACC	TCG	CAG	GTG	CGC	CAG
ATG	ACG	ACC	GCG	TCC	ACC	TCG	CAG	GTG	CGC	CAG
AAC	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATC	AAC
AAC	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATC	AAC
CGC	CAG	ATC	AAC	CTG	GAG	CTC	TAC	GCC	TCC	TAC
CGC	CAG	ATC	AAC	CTG	GAG	CTC	TAC	GCC	TCC	TAC
GTT	TAC	CTG	TCC	ATG	TCT	TAC	TAC	TTT	GAC	CGC
GTT	TAC	CTG	TCC	ATG	TCT	TAC	TAC	TTT	GAC	CGC
GAT	GAT	GTG	GCT	TTG	AAG	AAC	TTT	GCC	AAA	TAC
GAT	GAT	GTG	GCT	TTG	AAG	AAC	TTT	GCC	AAA	TAC
TTT	CTT	CAC	CAA	TCT	CAT	GAG	GAG	AGG	GAA	CAT
TTT	CTT	CAC	CAA	TCT	CAT	GAG	GAG	AGG	GAA	CAT
GCT	GAG	AAA	CTG	ATG	AAG	CTG	CAG	AAC	CAA	CGA
GCT	GAG	AAA	CTG	ATG	AAG	CTG	CAG	AAC	CAA	CGA
GGT	GGC	CGA	ATC	TTC	CTT	CAG	GAT	ATC	AAG	AAA
GGT	GGC	CGA	ATC	TTC	CTT	CAG	GAT	ATC	AAG	AAA
CCA	GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
CCA	GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
GCA	ATG	GAG	TGT	GCA	TTA	CAT	TTG	GAA	AAA	AAT
GCA	ATG	GAG	TGT	GCA	TTA	CAT	TTG	GAA	AAA	AAT
GTG	AAT	CAG	TCA	CTA	CTG	GAA	CTG	CAC	AAA	CTG
GTG	AAT	CAG	TCA	CTA	CTG	GAA	CTG	CAC	AAA	CTG
GCC	ACT	GAC	AAA	AAT	GAC	CCC	CAT	TTG	TGT	GAC
ATC	TCT	CCC	AGT	CCT	AGC	TGC	TGG	CAT	CAC	TAT

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TTC ATT GAG ACA CAT TAC CTG AAT GAG CAG GTG  
 ACT ACT AAC AGA CCG CAA CCT CAA CAC CAC CTT

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AAA GCC ATC AAA GAA TTG GGT GAC CAC GTG ACC  
 CTT CGA CCC CGC CGG AGG AAG AGA CCC CAT TCT

---

AAC TTG CGC AAG ATG GGA GCG CCC GAA TCT GGC  
 ATA CCA ACA CCT ATT CTG ATT TTT CGG TCA CCC

---

TTG GCG GAA TAT CTC TTT GAC AAG CAC ACC CTG  
 TGA AGTTTATATTCTTATCCTACCAGGCTTCGGAATAATCTCCCATATT

---

GGA GAC AGT GAT AAT GAA AGC TAA GCCTCGGGCTAATT  
 GTAACCTACTACTCCGGAAATCGCTGTGCGCTAACCGCTAACATTACTGC

---

TCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCGATGCAT  
 AGGCCACCTACTCATGCACCTAATTGGAAGCGCCACCCTAGCAATATCA

---

GCATGTTGGGGTTTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCAC  
 ACCATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTG

---

TTAAGTTCTTTGATTTGTACCATTCTTCAAATAAAGAAATTTGGTACCCA  
 ACTATCCTAGAAATCGCTGTGCGCTTAATCCAAGCCTACGTTTTCACT

---

AAAAAAA  
 TCTAGTAAGCCTCTACCTGCACGACAA<sup>C</sup>XACATAAAAA~~AAA~~

Fig. 2A Cont.

TTGACACCAGACCAACTGGTAATGGTAGCGACCGGGCGCTCAGCTGGAAATCCAAATAATGT

AATGCACACTCCATTGCATTCAGCCCGCCTCTCCTTAGTCGCCGCC

met	thr	thr	ala	ser	thr	ser	gln	val	arg	gln
ATG	ACG	ACC	GCG	TCC	ACC	TCG	CAG	GTG	CGC	CAG
asn	tyr	his	gln	asp	ser	glu	ala	ala	ile	asn
AAC	TAC	CAC	CAG	GAC	TCA	GAG	GCC	GCC	ATC	AAC
arg	gln	ile	asn	leu	glu	leu	tyr	ala	ser	tyr
CGC	CAG	ATC	AAC	CTG	GAG	CTC	TAC	GCC	TCC	TAC
val	tyr	leu	ser	met	ser	tyr	tyr	phe	asp	arg
GTT	TAC	CTG	TCC	ATG	TCT	TAC	TAC	TTT	GAC	CGC
asp	asp	val	ala	leu	lys	asn	phe	ala	lys	tyr
GAT	GAT	GTG	GCT	TTG	AAG	AAC	TTT	GCC	AAA	TAC
phe	leu	his	gln	ser	his	glu	glu	arg	gln	his
TTT	CTT	CAC	CAA	TCT	CAT	GAG	GAG	AGG	GAA	CAT
ala	glu	lys	leu	met	lys	leu	gln	asn	gln	arg
GCT	GAG	AAA	CTG	ATG	AAG	CTG	CAG	AAC	CAA	CGA
gly	gly	arg	ile	phe	leu	gln	asp	ile	lys	lys
GGT	GGC	CGA	ATC	TTC	CTT	CAG	GAT	ATC	AAG	AAA
pro	asp	cys	asp	asp	trp	glu	ser	gly	leu	asn
CCA	GAC	TGT	GAT	GAC	TGG	GAG	AGC	GGG	CTG	AAT
ala	met	glu	cys	ala	leu	his	leu	glu	lys	asn
GCA	ATG	GAG	TGT	GCA	TTA	CAT	TTG	GAA	AAA	AAT
val	asn	gln	ser	leu	leu	glu	phe	pro	ser	pro
GTG	AAT	CAG	TCA	CTA	CTG	GAA	TTC	CCT	TCT	CCT
ile	ser	pro	ser	pro	ser	cys	trp	his	his	thr
ATC	TCT	CCC	AGT	CCT	AGC	TGC	TGG	CAT	CAC	TAT
thr	thr	asn	arg	pro	glu	pro	gln	his	his	leu
ACT	ACT	AAC	AGA	CCG	CAA	CCT	CAA	CAC	CAC	CTT
leu	arg	pro	arg	arg	arg	lys	arg	pro	his	ser
CTT	CGA	CCC	CGC	CGG	AGG	AAG	AGA	CCC	CAT	TCT
ile	pro	thr	pro	ile	leu	ile	phe	arg	ser	pro
ATA	CCA	ACA	CCT	ATT	CTG	ATT	TTT	CGG	TCA	CCC

TGA AGTTTATATTCTTATCCTACCAGGCTTCGGAATAATCTCCCATATTGTAAGTTAC

TACTCCGGAAATCGCTGTCGCCTAACCGCTAACATTACTGCAGGCCACCTACTCATGCAC

CTAATTGGAAGCGCCACCCTAGCAATATCAACCATTAACTTCCTCTACACTTATCATC

TTCAAAATTCTAATTCTACTGACTATCCTAGAAATCGCTGTCGCCTTAATCCAAGCCTAC

GTTTTCACACTT~~TGTTA~~CCCAAAAAA

CTA GTAA GCCTCTA CCGCAC GACAA CAATATAA AAAAA Fig. 5

Fig. 5

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<sup>1061</sup> <u>TTGACACCAG</u>	<u>ACCAACTGGT</u>	<u>AATGGTAGCG</u>	<sup>BNC</sup> <u>ACCGGCGCTC</u>	<u>AGCTGGAATT</u>	<u>CCAAAAAATG</u>
<sup>NCS</sup> <u>TAATGCACAC</u>	<u>TCCATTGCAT</u>	TCAGCCCGCC	TCTCCTTAGT	CGCCGCCATG	ACGACCGCGT
CCACCTCGCA	GGTGCGCCAG	AACTACCACC	<sup>X1</sup> <u>AGGACTCAGA</u>	<u>GGCCGCCATG</u>	AACCGCCAGA
TCAACCTGGA	GCTCTACGCC	TCCTACGTTT	ACCTGTCCAT	GTCTTACTAC	<sup>17</sup> <u>TTTGACCGCG</u>
<sup>17</sup> <u>ATGATGTGGC</u>	<u>TTTGAAGAAG</u>	TTTGCCAAAT	ACTTTCTTCA	CCAATCTCAT	GAGGAGAGGG
AACATGCTGA	GAAACTGATG	AAGCTGCAGA	ACCAACGAGG	TGGCCGAATC	TTCCTTCAGG
ATATCAAGAA	ACCAGACTGT	GATGACTGGG	AGAG <sup>2.1</sup> <u>CGGGCT</u>	<u>GAATGCAATG</u>	<u>GAGTGTGCAT</u>
TACATTTGGA	AAAAAATGTG	AATCA <sup>ECOF</sup> <u>GTCACT</u>	<u>TACTGGAATT</u>	<u>CCCTTCTCCT</u>	ATCTCTCCCA
GTCCTAGCTG	CTGGCATCAC	TATACTACTA	ACAGACCGCA	ACCTCAACAC	CACCTTCTTC
GACCCCGCCG	GAGGAAGAGA	CCCCATTCTA	TACCAACACC	TATTCTGATT	TTTCGGTCAC
CCTGAAAGTTT	ATATTCTTAT	CCTACCAGGC	TTCGGAATAA	TCTCCCATAT	TGTAACCTAC
TACTCC <sup>SPF</sup> <u>GGAA</u>	<u>ATCGCTGTCT</u>	<u>CCTAACC</u> GCT	AACATTACTG	CAGGCCACCT	ACTCATGCAC
CTAATTG <sup>723</sup> <u>GAA</u>	<u>GCGCCACCCT</u>	<u>AGCAATATCA</u>	<u>ACCATTAACC</u>	TTCCCT <sup>767</sup> <u>TAC</u>	<u>ACTTATCATC</u>
<sup>767</sup> <u>TTTACAAATC</u>	<u>TAATTCTACT</u>	GAC <sup>16</sup> <u>TATCCTA</u>	<u>GAAATCGCTG</u>	<u>TCGCGTTAAT</u>	CCAAGCCTAC
GTITTCACAC	TTCTAGTAAG	<del>GCCTCTACCTG</del>	<del>GCACGACAACA</del>	<del>ACATAAAAAAA</del>	<del>AA</del>

Fig. 7

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TTGACACCAG	ACCAACTGGT	AATGGTAGCG	ACCGGCGCTC	AGCTGGAATT	CCAAAAAATG
TAATGCACAC	TCCATTGCAT	TCAGCCCGCC	TCTCCTTAGT	CGCCGCCAATG	ACGACCGCGT
CCACCTCGCA	GGTGCGCCAG	AACTACCACC	AGGACTCAGA	CGCCGCCATC	AACCGCCAGA
TCAACCTGGA	GCTCTACGCC	TCCTACGTTT	ACCTGTCCAT	GTCTTACTAC	TTTGACCGCG
ATGATGTGGC	TTTGAAGAAC	TTTGCCAAAT	ACTTTCTTCA	CCAATCTCAT	GAGGAGAGGG
AACATCCTGA	GAAACTGATG	<u>PstI</u> AAGCTGCGA	ACCAACGAGG	TGGCCGAATC	TTCTTCAGG
ATATCAAGAA	ACCAGACTGT	GATGACTGGG	AGAGCGGGCT	GAATGCAATG	GAGTGTGCAT
TACATTTGGA	AAAAAATGTG	AATCAGTCAC	<u>ECOR1</u> TACGGGAATT	CCCTTCTCCT	ATCTCTCCCA
GTCTAGCTG	CTGGCATCAC	TATACTACTA	ACAGACCGCA	ACCTCAACAC	CACCTTCTTC
GACCCCGCCG	GAGGAAGAGA	CCCCATTCTA	TACCAACACC	TAITCTGATT	TTTCGGTCAC
<del>CCCTG</del> AGTTT	ATATTCTTAT	CCTACCAGGC	TTCGGAATAA	TCTCCCATAT	TGTAACTTAC
TACTCCGGAA	ATCGCTGTCTG	CCTAACCGCT	AACATTACTG	CAGGCCACCT	ACTCATGCAC
CTAATTGGAA	GCGCCACCCT	AGCAATATCA	ACCATTAAACC	TTCCCTCTAC	ACTTATCATC
TTCACAATTC	TAATTCTACT	GACTATCCTA	GAAATCGCTG	TCGCCTTAAT	CCAAGCCTAC
GTTTTACAC	TTCTAGTAA	<del>CCCTCTACCTG</del>	<del>GCACGACAACA</del>	<del>CATAAAAAA</del>	<del>A</del>

Fig. 8